

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/016,159

DATE: 01/27/1999
TIME: 15:14:04

INPUT SET: S30362.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Lee, Jong Y.

(ii) TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Fish & Richardson P.C., P.A.
- (B) STREET: 60 South Sixth Street, Suite 3300
- (C) CITY: Minneapolis
- (D) STATE: MN
- (E) COUNTRY: USA
- (F) ZIP: 55402

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/016,159
- (B) FILING DATE: 30-JAN-1998

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/876,227
- (B) FILING DATE: 16-JUN-1997

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/734,097
- (B) FILING DATE: 21-OCT-1996

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/460,525
- (B) FILING DATE: 02-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Ellinger, Mark S.
- (B) REGISTRATION NUMBER: 34,812
- (C) REFERENCE/DOCKET NUMBER: 07004/002003

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47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: 612/335-5070

49 (B) TELEFAX: 612/288-9696

50

51

52 (2) INFORMATION FOR SEQ ID NO:1:

53

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 23 base pairs

56 (B) TYPE: nucleic acid

57 (C) STRANDEDNESS: single

58 (D) TOPOLOGY: linear

59

60 (ii) MOLECULE TYPE: synthetic DNA

61

62 (iii) HYPOTHETICAL: NO

63

64 (iv) ANTI-SENSE: NO

65

66

67 (ix) FEATURE:

68 (A) NAME/KEY: BamH1 linker ar 5' end followed by sequence for amino

69 acids 25 through 29 of the full length human EpOR protein. Forward primer for

70 Sequence ID No. 2."

71

72

73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

74

75 TTGGATCC GCG CCC CCG CCT A AC

23

76 Ala Pro Pro Pro

77

1

78

79 (2) INFORMATION FOR SEQ ID NO:2:

80

81 (i) SEQUENCE CHARACTERISTICS:

82 (A) LENGTH: 22 base pairs

83 (B) TYPE: nucleic acid

84 (C) STRANDEDNESS: single

85 (D) TOPOLOGY: linear

86

87 (ii) MOLECULE TYPE: synthetic DNA

88

89 (iii) HYPOTHETICAL: NO

90

91 (iv) ANTI-SENSE: NO

92

93

94 (ix) FEATURE:

95 (A) NAME/KEY: EcoR1 linker followed by sequence complementary to

96 coding sequence for amino acids 226 through 222 of full length human EpOR

97 protein. Reverse primer for Sequence ID No. 1.

98

99

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100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
101
102 TGAATTCGGG GTCCAGGTCG CT 22
103
104 (2) INFORMATION FOR SEQ ID NO:3:
105
106 (i) SEQUENCE CHARACTERISTICS:
107 (A) LENGTH: 18 base pairs
108 (B) TYPE: nucleic acid
109 (C) STRANDEDNESS: double
110 (D) TOPOLOGY: linear
111
112 (ii) MOLECULE TYPE: other nucleic acid
113
114 (iii) HYPOTHETICAL: NO
115
116 (iv) ANTI-SENSE: NO
117
118 (vi) ORIGINAL SOURCE:
119 (A) ORGANISM: Homo sapiens
120
121 (vii) IMMEDIATE SOURCE:
122 (B) CLONE: pGEX-2T, Pharmacia (Mechanicsburg, PA)
123
124 (ix) FEATURE:
125 (A) NAME/KEY: Thrombin Cleavage Site in plasmid vector pGEX-2T."
126
127 (x) PUBLICATION INFORMATION:
128 (A) AUTHORS: Smith, D.B.
129 Johnson, K.S.
130 (B) TITLE: Single-step purification of polypeptides
131 expressed in Escherichia coli as fusions with
132 glutathione-S-transferase
133 (D) VOLUME: 67
134 (F) PAGES: 31-40
135 (G) DATE: 1988
136
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
138
139 CTG GTT CCG CGT GGA T CC 18
140 Leu Val Pro Arg Gly
141 5
142
143 (2) INFORMATION FOR SEQ ID NO:4:
144
145 (i) SEQUENCE CHARACTERISTICS:
146 (A) LENGTH: 1527 base pairs
147 (B) TYPE: nucleic acid
148 (C) STRANDEDNESS: double
149 (D) TOPOLOGY: linear
150
151
152 (x) PUBLICATION INFORMATION:

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153      (A) AUTHORS: Winkelmann , J. C., et al.
154      (C) JOURNAL: Blood
155      (D) VOLUME: 76
156      (E) ISSUE: 1
157      (F) PAGES: 24-30
158      (G) DATE: 1990
159      (x) PUBLICATION INFORMATION:
160      (A) AUTHORS: Jones, S.S., et al.
161      (C) JOURNAL: Blood
162      (D) VOLUME: 76
163      (E) ISSUE: 1
164      (F) PAGES: 31-35
165      (G) DATE: 1990
166      (x) PUBLICATION INFORMATION:
167      (A) AUTHORS: Noguchi, C.T., et al.
168      (C) JOURNAL: Blood
169      (D) VOLUME: 78
170      (E) ISSUE: 10
171      (F) PAGES: 2548-2556
172      (G) DATE: 1991
173
174      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
175
176      ATG GAC CAC CTC GGG GCG TCC CTC TGG CCC CAG GTC GGC TCC CTT TGT      48
177      Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys
178      1          5          10          15
179
180      CTC CTG CTC GCT GGG GCC GCC TGG GCG CCC CCG CCT AAC CTC CCG GAC      96
181      Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp
182      20          25          30
183
184      CCC AAG TTC GAG AGC AAA GCG GCC TTG CTG GCG GCC CGG GGG CCC GAA      144
185      Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu
186      35          40          45
187
188      GAG CTT CTG TGC TTC ACC GAG CGG TTG GAG GAC TTG GTG TGT TTC TGG      192
189      Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp
190      50          55          60
191
192      GAG GAA GCG GCG AGC GCT GGG GTG GGC CCG GGC AAC TAC AGC TTC TCC      240
193      Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser
194      65          70          75          80
195
196      TAC CAG CTC GAG GAT GAG CCA TGG AAG CTG TGT CGC CTG CAC CAG GCT      288
197      Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala
198      85          90          95
199
200      CCC ACG GCT CGT GGT GCG GTG CGC TTC TGG TGT TCG CTG CCT ACA GCC      336
201      Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala
202      100          105          110
203
204      GAC ACG TCG AGC TTC GTG CCC CTA GAG TTG CGC GTC ACA GCA GCC TCC      384
205      Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser

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	115	120	125	
206				
207				
208	GGC GCT CCG CGA TAT CAC CGT GTC ATC CAC ATC AAT GAA GTA GTG CTC			432
209	Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu			
210	130	135	140	
211				
212	CTA GAC GCC CCC GTG GGG CTG GTG GCG CGG TTG GCT GAC GAG AGC GGC			480
213	Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly			
214	145	150	155	160
215				
216	CAC GTA GTG TTG CGC TGG CTC CCG CCG CCT GAG ACA CCC ATG ACG TCT			528
217	His Val Val Leu Arg Trp Leu Pro Pro Glu Thr Pro Met Thr Ser			
218	165	170	175	
219				
220	CAC ATC CGC TAC GAG GTG GAC GTC TCG GCC GGC AAC GGC GCA GGG AGC			576
221	His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser			
222	180	185	190	
223				
224	GTA CAG AGG GTG GAG ATC CTG GAG GGC CGC ACC GAG TGT GTG CTG AGC			624
225	Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser			
226	195	200	205	
227				
228	AAC CTG CGG GGC CGG ACG CGC TAC ACC TTC GCC GTC CTC GCG CGT ATG			672
229	Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Leu Ala Arg Met			
230	210	215	220	
231				
232	GCT GAG CCG AGC TTC GGC GGC TTC TGG AGC GCC TGG TCG GAG CCT GTG			720
233	Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val			
234	225	230	235	240
235				
236	TCG CTG CTG ACG CCT AGC GAC CTG GAC CCC CTC ATC CTG ACG CTC TCC			768
237	Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser			
238	245	250	255	
239				
240	CTC ATC CTC GTG GTC ATC CTG GTG CTG CTG ACC GTG CTC GCG CTG CTC			816
241	Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu			
242	260	265	270	
243				
244	TCC CAC CGC CGG GCT CTG AAG CAG AAG ATC TGG CCT GGC ATC CCG AGC			864
245	Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser			
246	275	280	285	
247				
248	CCA GAG AGC GAG TTT GAA GGC CTC TTC ACC ACC CAC AAG GGT AAC TTC			912
249	Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe			
250	290	295	300	
251				
252	CAG CTG TGG CTG TAC CAG AAT GAT GGC TGC CTG TGG TGG AGC CCC TGC			960
253	Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys			
254	305	310	315	320
255				
256	ACC CCC TTC ACG GAG GAC CCA CCT GCT TCC CTG GAA GTC CTC TCA GAG			1008
257	Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu			
258	325	330	335	

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. §§ 1.821-1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990, and at 55 FR 18230, May 1, 1990.
- ☒ 2. This application does not contain, as a **separate part of the disclosure** on paper copy, a "Sequence Listing" as required by 37 C.F.R. § 1.821(c).
- ☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. § 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. §§ 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing".
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 C.F.R. § 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. § 1.821(e).
- ☒ 7. Other:

A paper copy sequence listing was filed with the application. However, no computer-readable copy or request that the Office prepare such copy from the listing filed in the parent application (37 C.F.R. § 1.821(e)) was received. Additionally, no amendment directing entry of the sequence listing into the specification was submitted.

Applicant must provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ ~~An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry of the sequence listing into the specification.~~
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. § 1.821(e) or § 1.821(f) or § 1.821(g) or § 1.825(b) or § 1.825(d).

For questions regarding compliance with these requirements, please contact one of the following:

For rules interpretation, call (703) 308-4216.

For CRF submission help, call (703) 308-4212.

For PatentIn software help, call (703) 557-0400.

Please return a copy of this notice with your response.